

SUPPLEMENTARY MATERIAL

Supplemental Figure S1. Expression patterns of transcription factors and key target genes in early T-cell precursors. Data are downloaded from www.immgen.org (Mingueneau et al. 2013) from the “Microarray v1” datasets; thymocyte subsets from ETP through commitment (violet line) and into β -selection, credited to T. Kreslavsky. (A) Expression patterns of genes encoding the E proteins E2A and HEB; TCF1; GATA3; Bcl11b; Ets1; Runx1; PU.1; and the canonical Notch-induced transcriptional repressor HES1, the most consistently expressed reporter for the strength of Notch signaling. (B) Expression of key T-lineage differentiation genes and growth factor receptors with roles in T-cell development. Shown are the differentiation genes encoding the CD3 γ , δ , and ϵ signaling chains that assemble with the T-cell receptor complex; the surrogate TCR chain (Ptcra) that complexes with newly-expressed TCR β chains for β -selection; the recombinase protein RAG1; and the TCR-signaling kinases ZAP70 and ITK (another kinase, LCK, is expressed at high levels already from the ETP stage). Also shown are the genes encoding the stem/progenitor cell growth factor receptor c-Kit (repressed by Bcl11b); the IL-2 receptor α chain, also called CD25, that acts as the main surface marker for the DN2 and DN3 stages (positively regulated by TCF1 and Notch signals); and the IL-7 receptor, the main growth factor receptor that expands the early pro-T cells. E protein target genes are shown in red and orange colors.

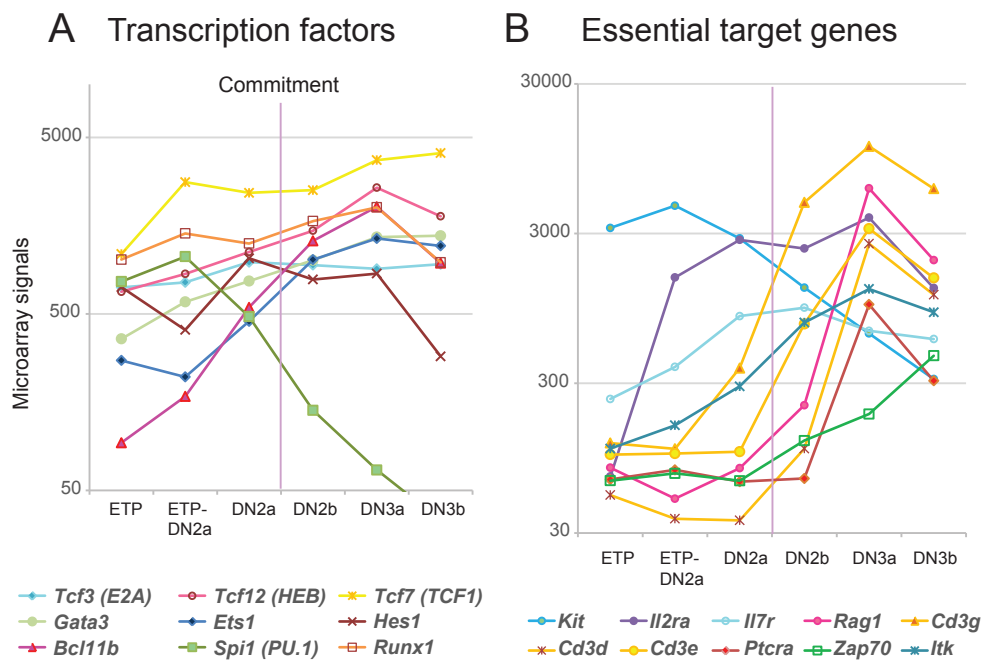


Fig. S1